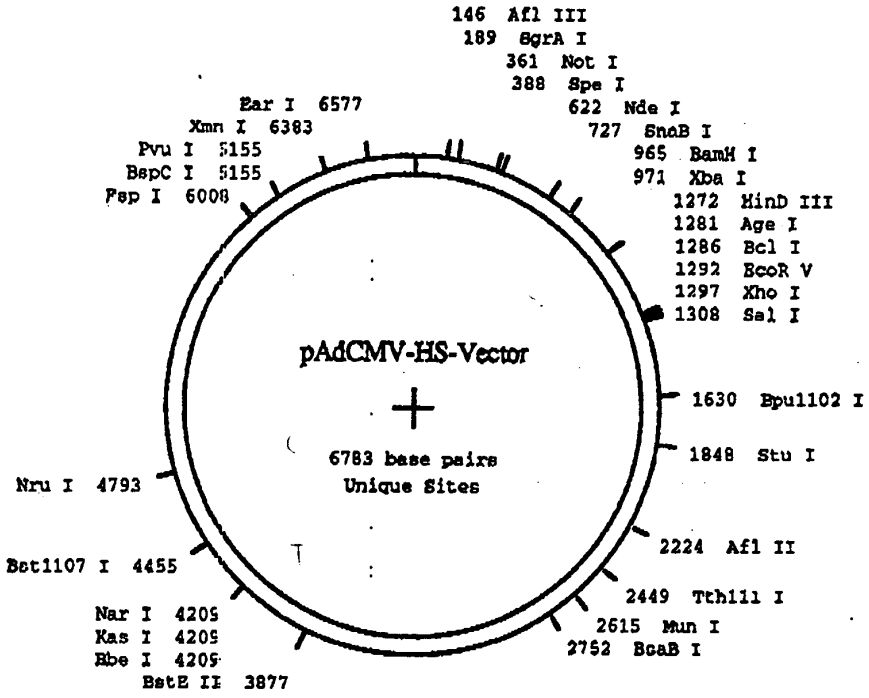

146 Afl III
189 SgrA I
361 Not I
388 Spe I
622 Nde I
727 SnaB I
965 BamH I
971 Xba I
1272 HinD III
1281 Age I
1286 Bcl I
1292 EcoR V
1297 Xho I
1308 Sal I
1630 Bpu1102 I
1848 Stu I
2224 Afl II
2449 Tth111 I
2615 Mun I
2752 BsaB I
Ear I 6577
Xmn I 6383
Pvu I 5155
BspC I 5155
Fsp I 6008
Nru I 4793
Bst1107 I 4455
Nar I 4209
Kas I 4209
Bbe I 4209
BstE II 3877
pAdCMV-HS-Vector
6783 base pairs
Unique Sites

Figure 1(a)

Figure 1 **AdCMV-HS -Vector**

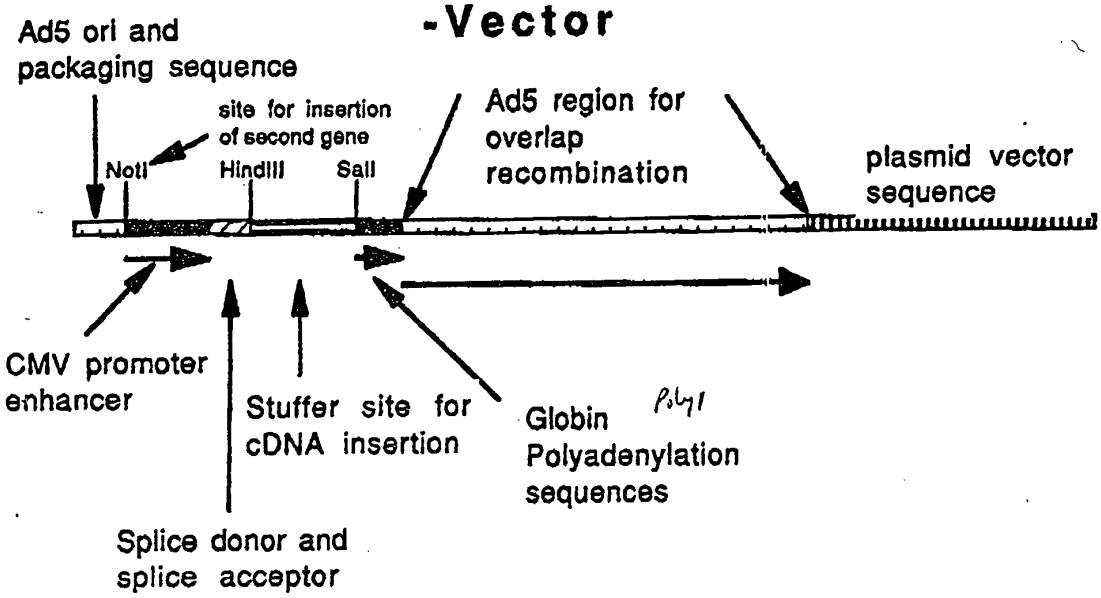


Figure 1(b)

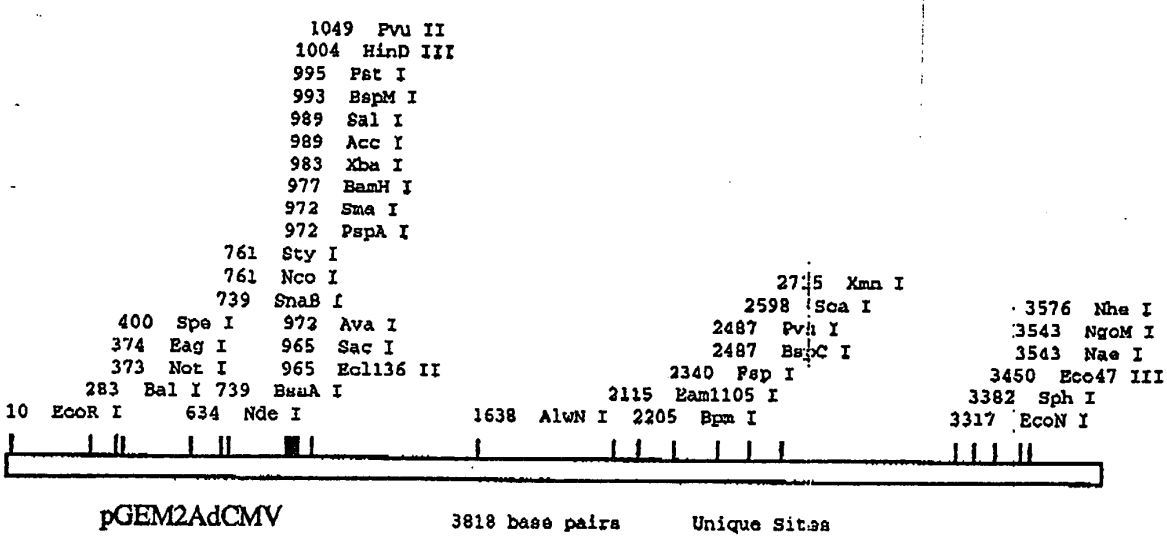

1049 Pvu II
1004 HinD III
995 Pst I
993 BspM I
989 Sal I
989 Acc I
983 Xba I
977 BamH I
972 Sma I
972 PspA I
761 Sty I
761 Nco I
739 SnaB I
400 Spe I
374 Eag I
373 Not I
283 Bal I
739 BsaA I
10 EcoR I
634 Nde I
972 Ava I
965 Sac I
965 Ecl136 II
1638 AlwN I
2115 Eam1105 I
2205 Bpm I
2340 Fsp I
2487 Pvu I
2487 BspC I
2598 Sca I
2715 Xmn I
3317 EcoN I
3382 Sph I
3450 Eco47 III
3543 Nae I
3543 NgoM I
3576 Nhe I
pGEM2AdCMV
3818 base pairs
Unique Sites

Figure 2

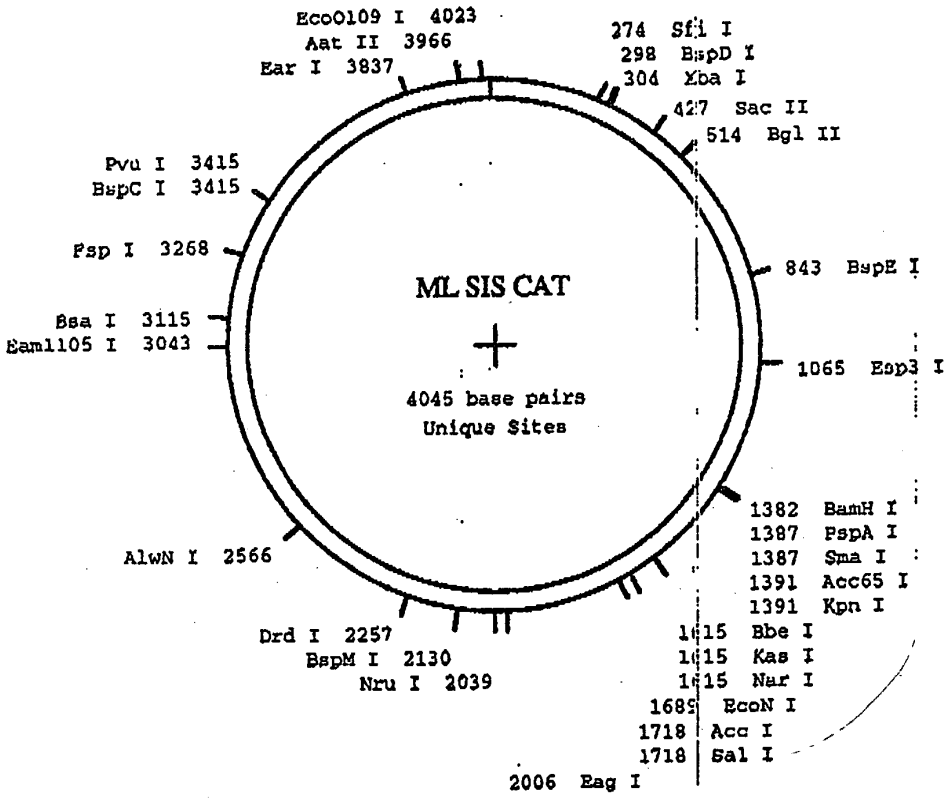

ML SIS CAT
4045 base pairs
Unique Sites
EcoO109 I 4023
Aat II 3966
Ear I 3837
Pvu I 3415
BspC I 3415
Fsp I 3268
Bsa I 3115
Bam1105 I 3043
AlwN I 2566
Drd I 2257
BspM I 2130
Nru I 2039
274 Sfi I
298 BspD I
304 Xba I
427 Sac II
514 Bgl II
843 BspE I
1065 Esp3 I
1382 BamH I
1387 PspA I
1387 Sma I
1391 Acc65 I
1391 Kpn I
1615 Bbe I
1615 Kas I
1615 Nar I
1689 EcoN I
1718 Acc I
1718 Sal I
2006 Eag I

Figure 3

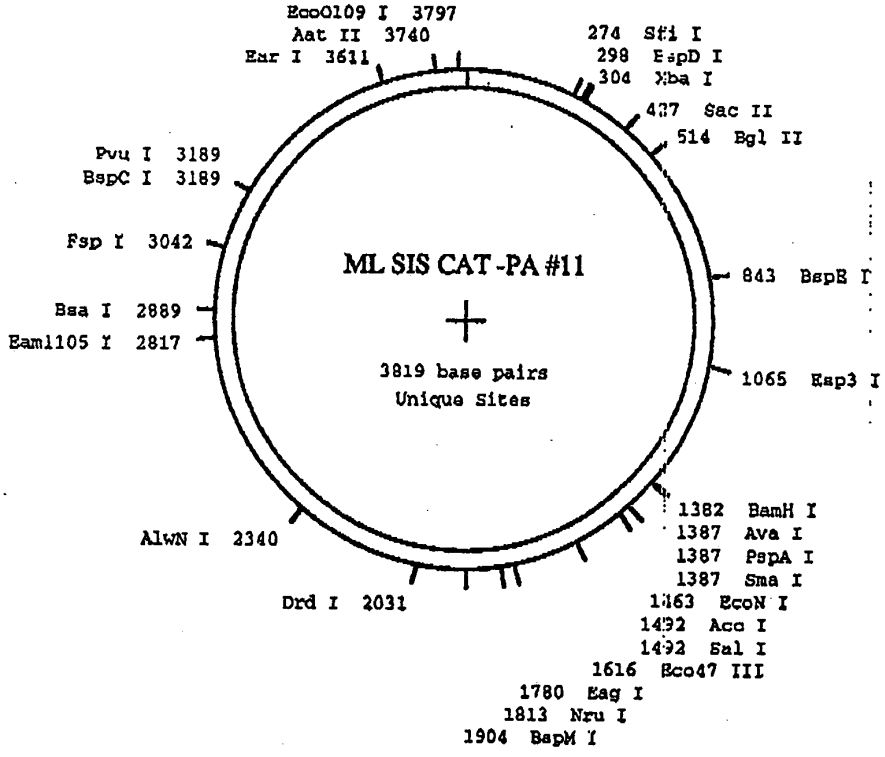

Eco0109 I 3797
Aat II 3740
Ear I 3611
274 Sfi I
298 EspD I
304 Xba I
437 Sac II
514 Bgl II
Pvu I 3189
BspC I 3189
Fsp I 3042
ML SIS CAT-PA #11
843 BspE I
Bsa I 2889
Eam1105 I 2817
3819 base pairs
Unique Sites
1065 Esp3 I
1382 BamH I
1387 Ava I
1387 PspA I
1387 Sma I
AlwN I 2340
1463 EcoN I
1492 Acc I
1492 Sal I
1616 Eco47 III
Drd I 2031
1780 Eag I
1813 Nru I
1904 BspM I

Figure 4

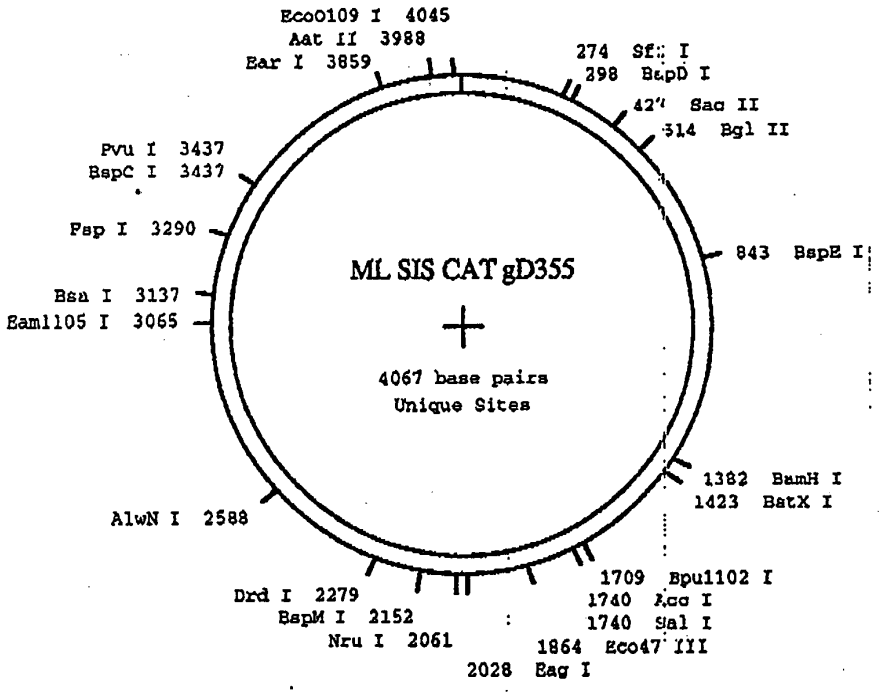

Eco0109 I 4045
Aat II 3988
Ear I 3859
274 Sfi I
298 BspD I
42? Sac II
514 Bgl II
Pvu I 3437
BspC I 3437
Fsp I 3290
843 BspE I
ML SIS CAT gD355
Bsa I 3137
Eam1105 I 3065
4067 base pairs
Unique Sites
1382 BamH I
1423 BstX I
AlwN I 2588
1709 Bpu1102 I
1740 Acc I
1740 Sal I
Drd I 2279
BspM I 2152
Nru I 2061
1864 Eco47 III
2028 Eag I

Figure 5

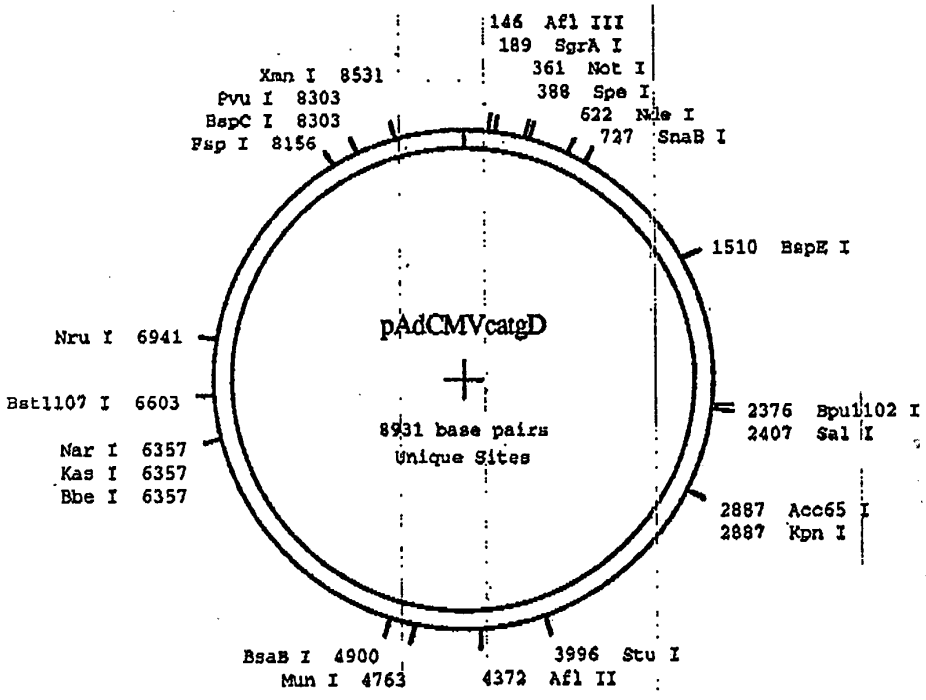

146 Afl III
189 SgrA I
361 Not I
388 Spe I
622 Nde I
727 SnaB I
1510 BspE I
2376 Bpu1102 I
2407 Sal I
2887 Acc65 I
2887 Kpn I
3996 Stu I
4372 Afl II
BsaB I 4900
Mun I 4763
Nru I 6941
Bst1107 I 6603
Nar I 6357
Kas I 6357
Bbe I 6357
Xmn I 8531
Pvu I 8303
BspC I 8303
Fsp I 8156
pAdCMVcatgD
8931 base pairs
Unique Sites

Figure 6

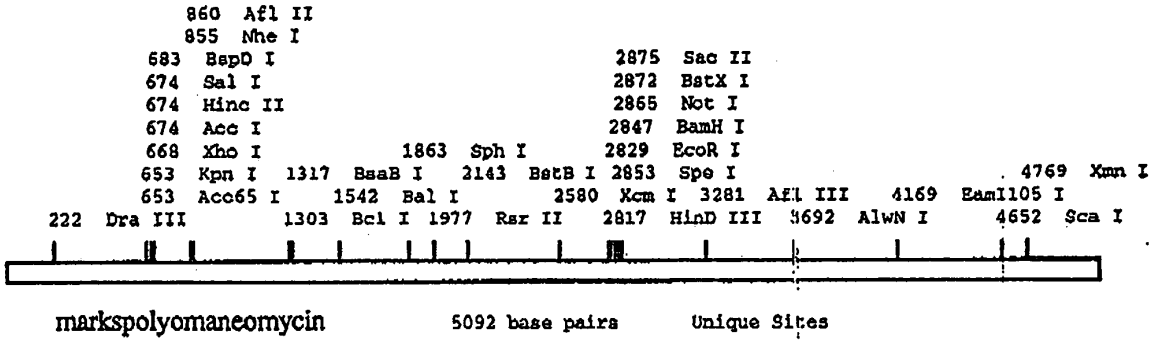

860 Afl II
855 Nhe I
683 BspD I
674 Sal I
674 Hinc II
674 Acc I
668 Xho I
653 Kpn I
653 Acc65 I
222 Dra III
1303 Bcl I
1317 BsaB I
1542 Bal I
1863 Sph I
1977 Rsr II
2143 BstB I
2580 Xcm I
2817 HinD III
2829 EcoR I
2847 BamH I
2853 Spe I
2865 Not I
2872 BstX I
2875 Sac II
3281 Afl III
3692 AlwN I
4169 BamI105 I
4652 Sca I
4769 Xmn I
markspolyomaneomycin
5092 base pairs
Unique Sites

Figure 7

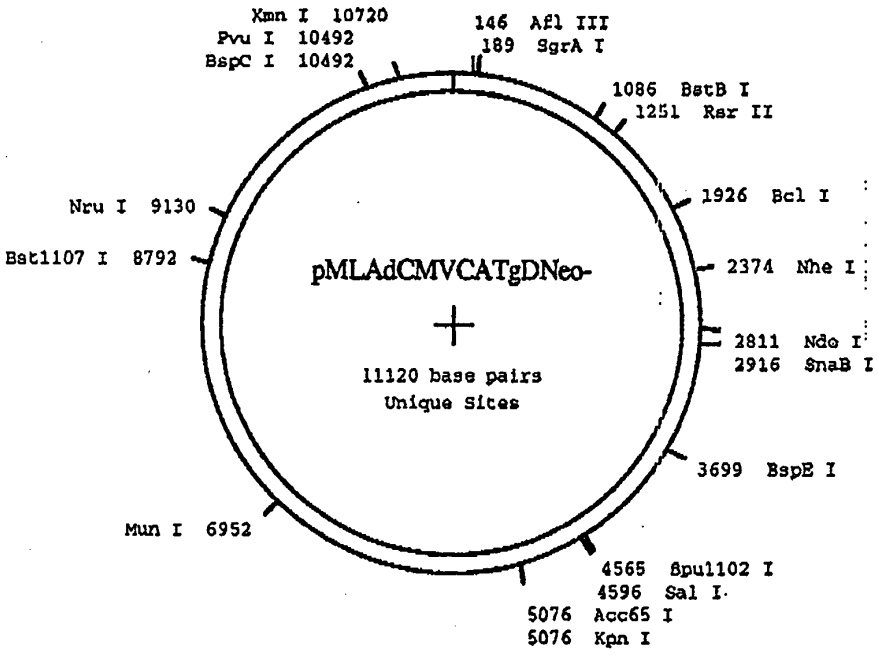

Xmn I 10720
Pvu I 10492
BspC I 10492
146 Afl III
189 SgrA I
1086 BstB I
1251 Rsr II
1926 Bcl I
2374 Nhe I
2811 Ndo I
2916 SnaB I
3699 BspE I
4565 Spu1102 I
4596 Sal I
5076 Acc65 I
5076 Kpn I
Mun I 6952
Bst1107 I 8792
Nru I 9130
pMLAdCMVCATgDNeo-
11120 base pairs
Unique Sites

Figure 8

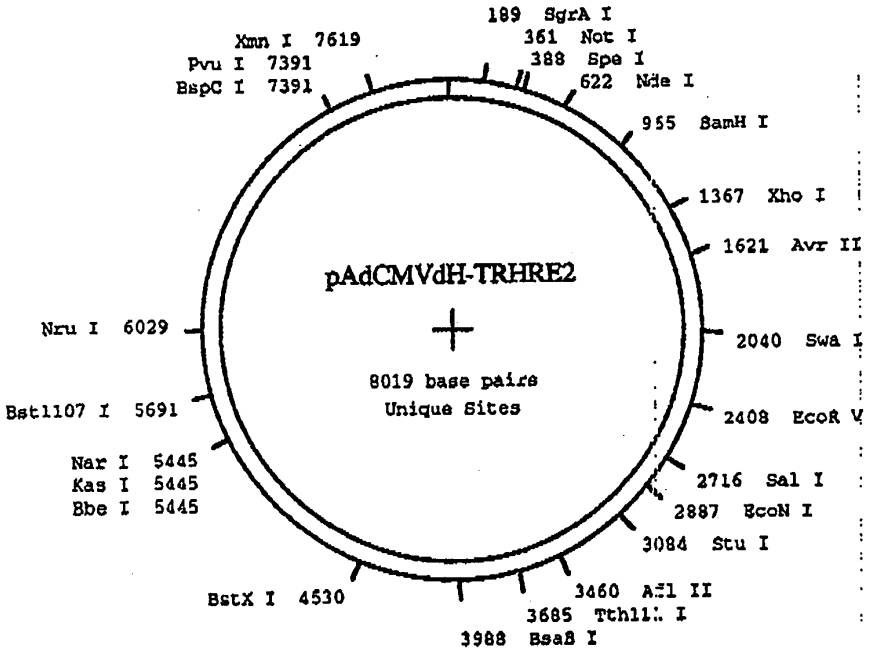

189 SgrA I
361 Not I
388 Spe I
622 Nde I
955 BamH I
1367 Xho I
1621 Avr II
2040 Swa I
2408 EcoR V
2716 Sal I
2887 EcoN I
3084 Stu I
3460 Afl II
3685 Tth111 I
3988 BsaB I
BstX I 4530
Bst1107 I 5691
Nar I 5445
Kas I 5445
Bbe I 5445
Nru I 6029
Xmn I 7619
Pvu I 7391
BspC I 7391
pAdCMVdH-TRHRE2
8019 base pairs
Unique Sites

Figure 9

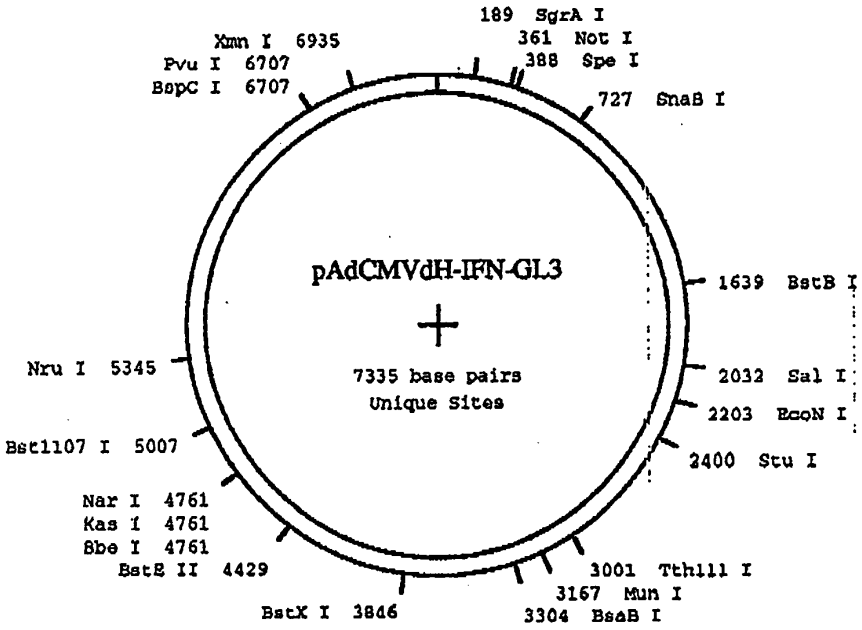

189 SgrA I
361 Not I
388 Spe I
727 SnaB I
1639 BstB I
2032 Sal I
2203 EcoN I
2400 Stu I
3001 Tth111 I
3167 Mun I
3304 BsaB I
3846 BstX I
4429 BstE II
4761 Nar I
4761 Kas I
4761 Sbe I
5007 Bst1107 I
5345 Nru I
6707 BspC I
6707 Pvu I
6935 Xmn I
pAdCMVdH-IFN-GL3
7335 base pairs
Unique Sites

Figure 10

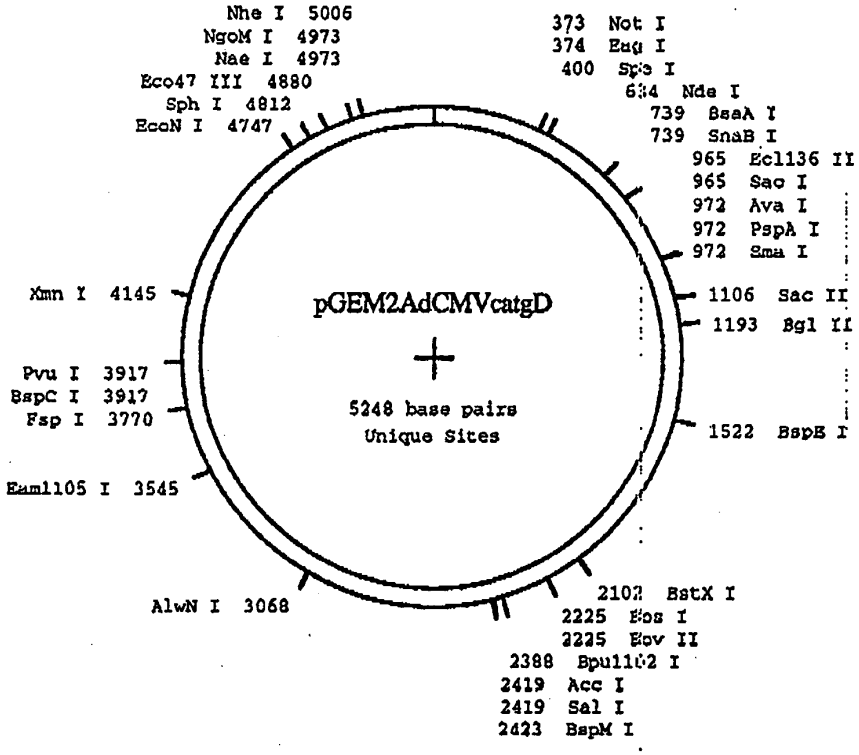

Nhe I 5006
NgoM I 4973
Nae I 4973
Eco47 III 4880
Sph I 4812
EcoN I 4747
373 Not I
374 Eag I
400 Sfo I
634 Nde I
739 BseA I
739 SnaB I
965 Ecl136 II
965 Sac I
972 Ava I
972 PspA I
972 Sma I
1106 Sac II
1193 Bgl II
1522 BspE I
2102 BstX I
2225 Eos I
2225 Eov II
2388 Bpu1102 I
2419 Acc I
2419 Sal I
2423 BspM I
AlwN I 3068
Eam1105 I 3545
Pvu I 3917
BspC I 3917
Fsp I 3770
Xmn I 4145
pGEM2AdCMVcatgD
5248 base pairs
Unique Sites

Figure 11

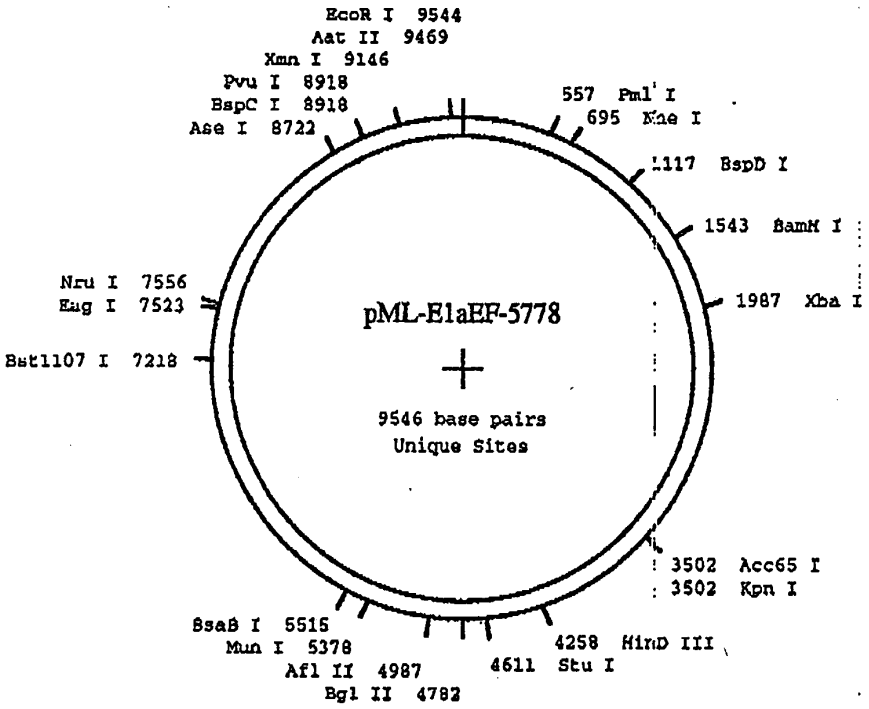

EcoR I 9544
Aat II 9469
Xmn I 9146
Pvu I 8918
BspC I 8918
Ase I 8722
557 Pml I
695 Nae I
1117 BspD I
1543 BamH I
1987 Xba I
3502 Acc65 I
3502 Kpn I
4258 HinD III
4611 Stu I
Bgl II 4782
Afl II 4987
Mun I 5378
BsaB I 5515
Bst1107 I 7218
Eag I 7523
Nru I 7556
pML-E1aEF-5778
9546 base pairs
Unique Sites

Figure 12

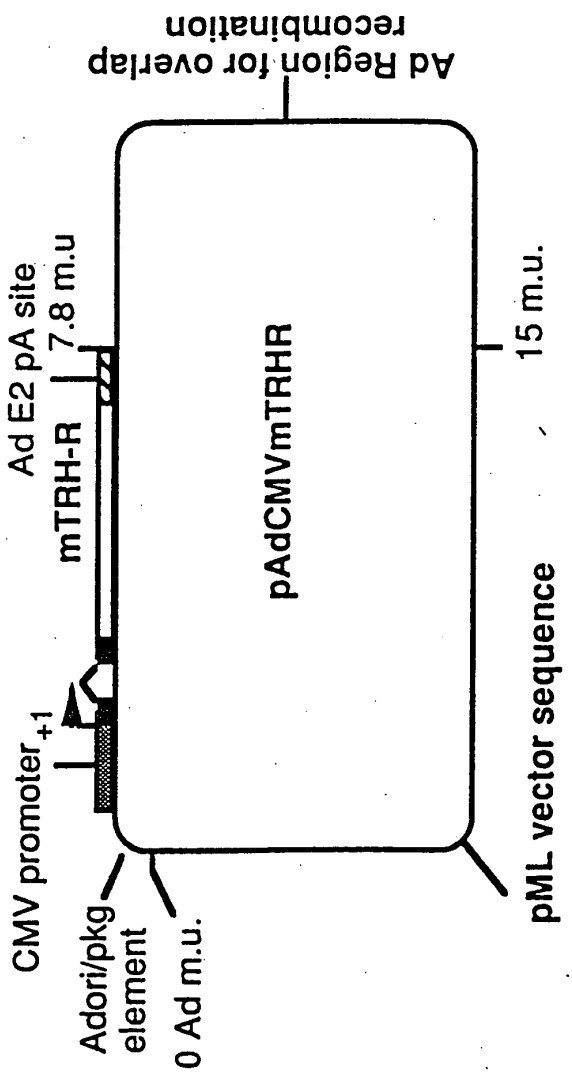

Ad Region for overlap recombination
Ad E2 pA site
7.8 m.u
mTRH-R
pAdCMVmTRHR
15 m.u.
CMV promoter +1
Adori/pkg element
0 Ad m.u.
pML vector sequence

Figure 13

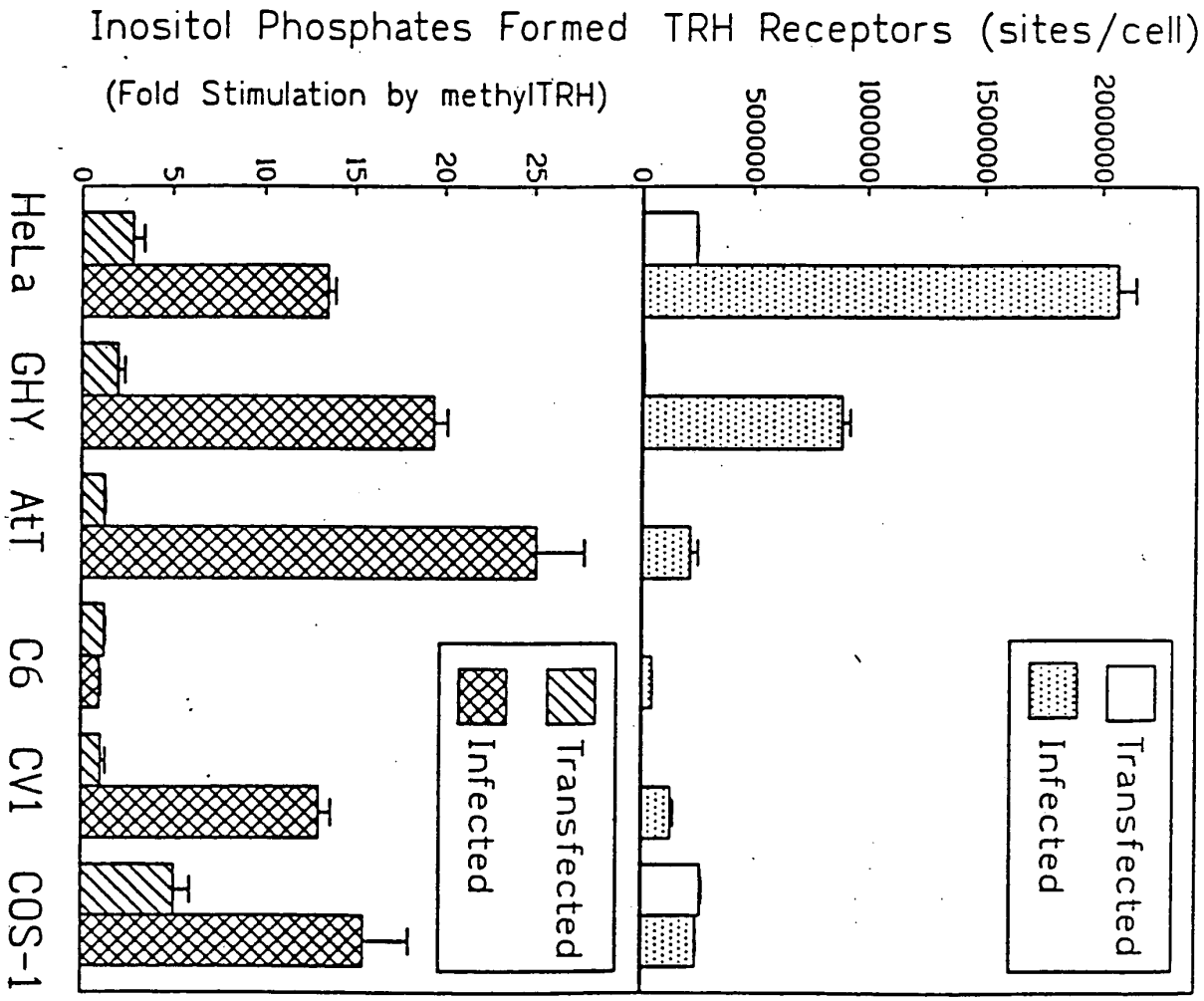

Inositol Phosphates Formed
(Fold Stimulation by methylTRH)
0
5
10
15
20
25
TRH Receptors (sites/cell)
0
500000
1000000
1500000
2000000
HeLa
GHY
AtT
C6
CV1
COS-1
Transfected
Infected
Transfected
Infected

Figure 14

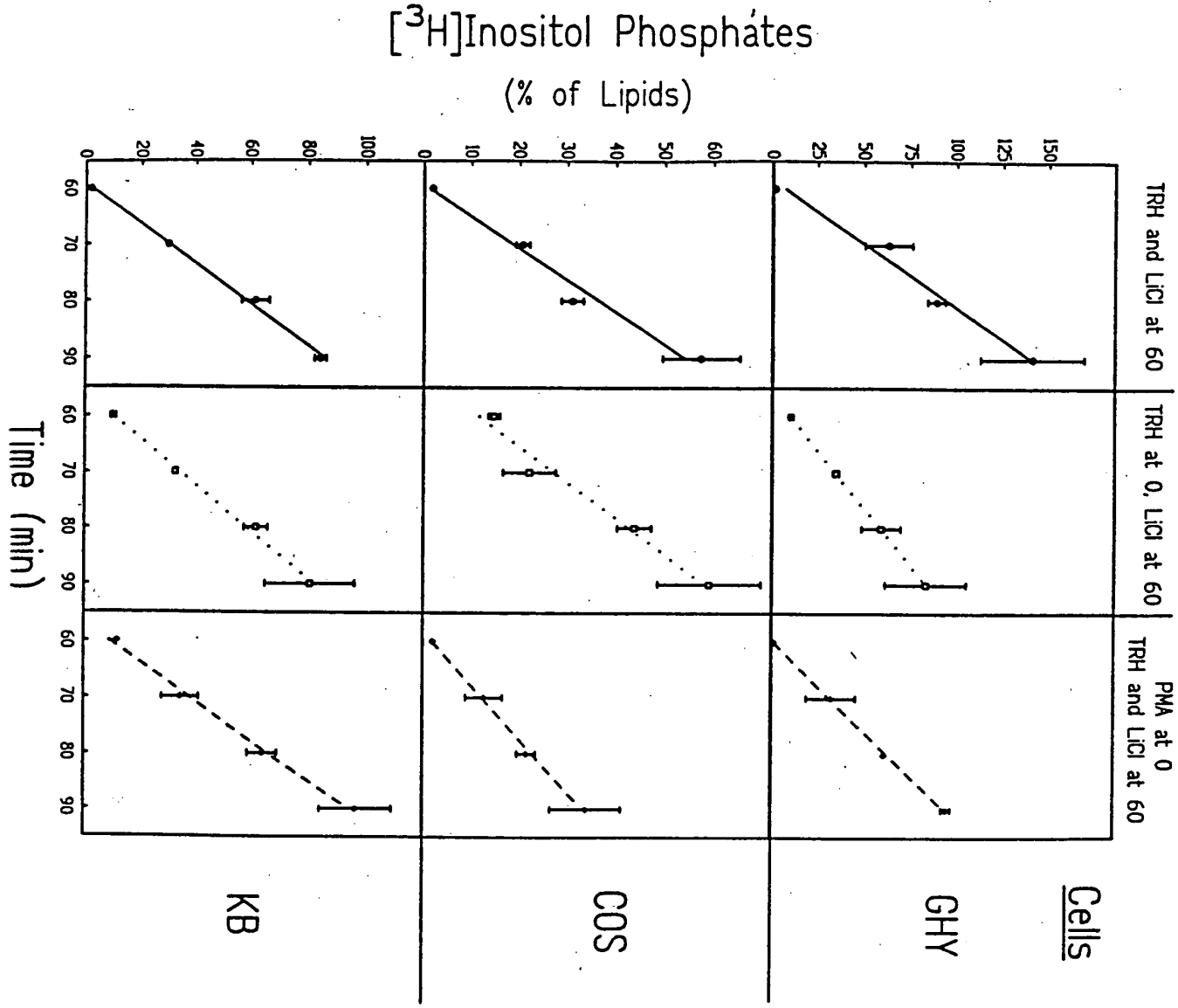

[3H]Inositol Phosphates
(% of Lipids)
Time (min)
Cells
GHY
COS
KB
TRH and LiCl at 60
TRH at 0, LiCl at 60
PMA at 0
TRH and LiCl at 60

Figure 15

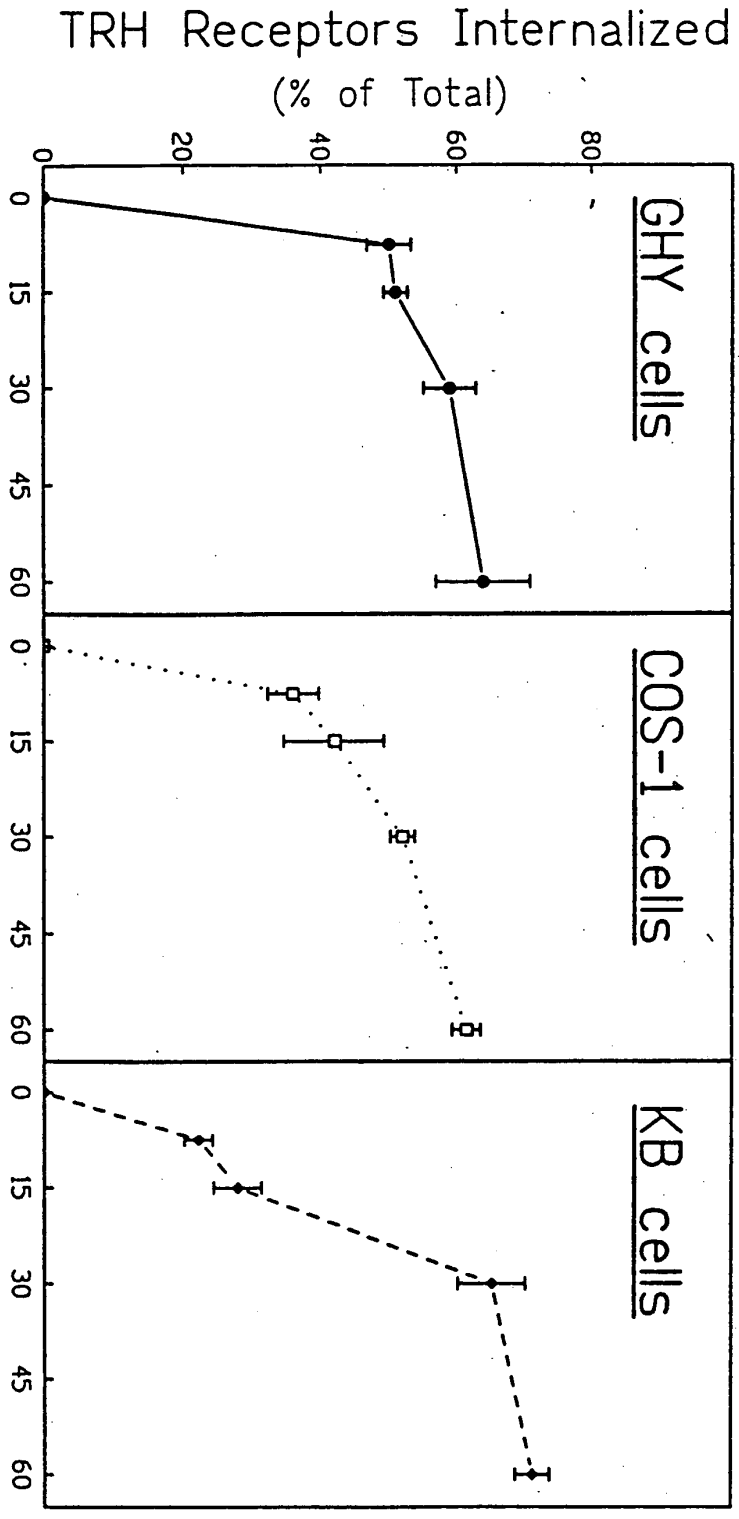

TRH Receptors Internalized
(% of Total)
0
20
40
60
80
GHY cells
COS-1 cells
KB cells
0
15
30
45
60
Time (min)

Figure 16

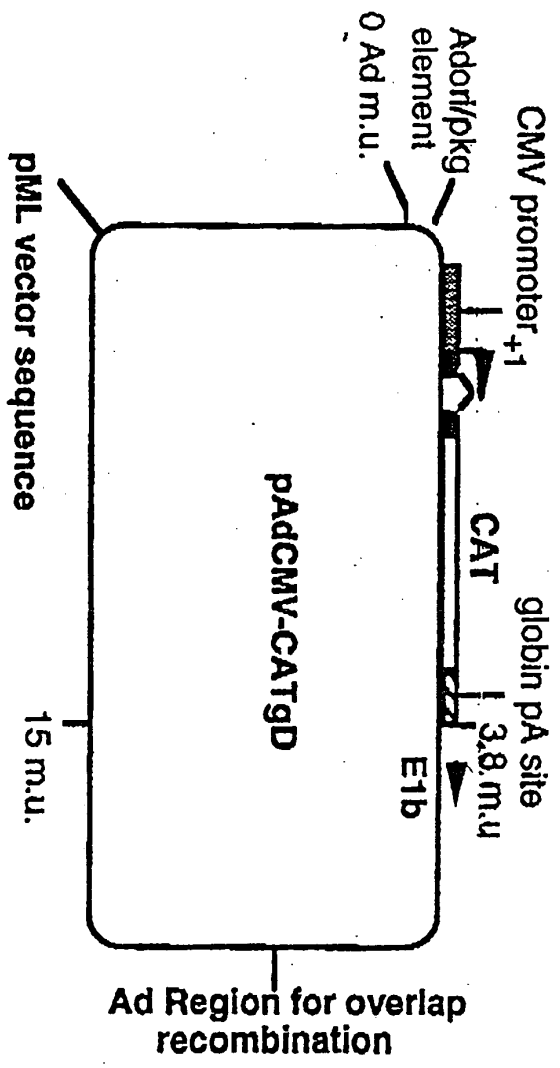

0 Ad m.u.
Adorf/pkg element
CMV promoter
+1
pML vector sequence
pAdCMV-CATgD
CAT
globin pA site
3.8 m.u
E1b
15 m.u.
Ad Region for overlap recombination

FIGURE 17

08/166925

FETAL CARDIOCYTES

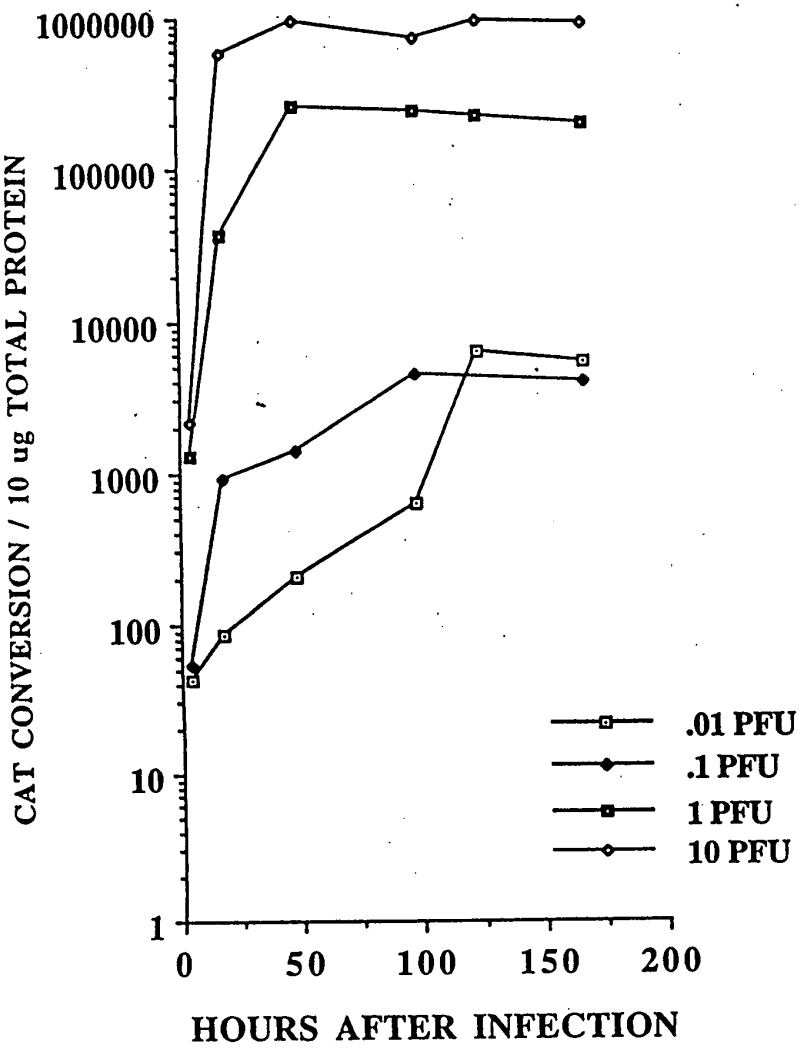


Figure 18(a)

ADULT CARDIOCYTES

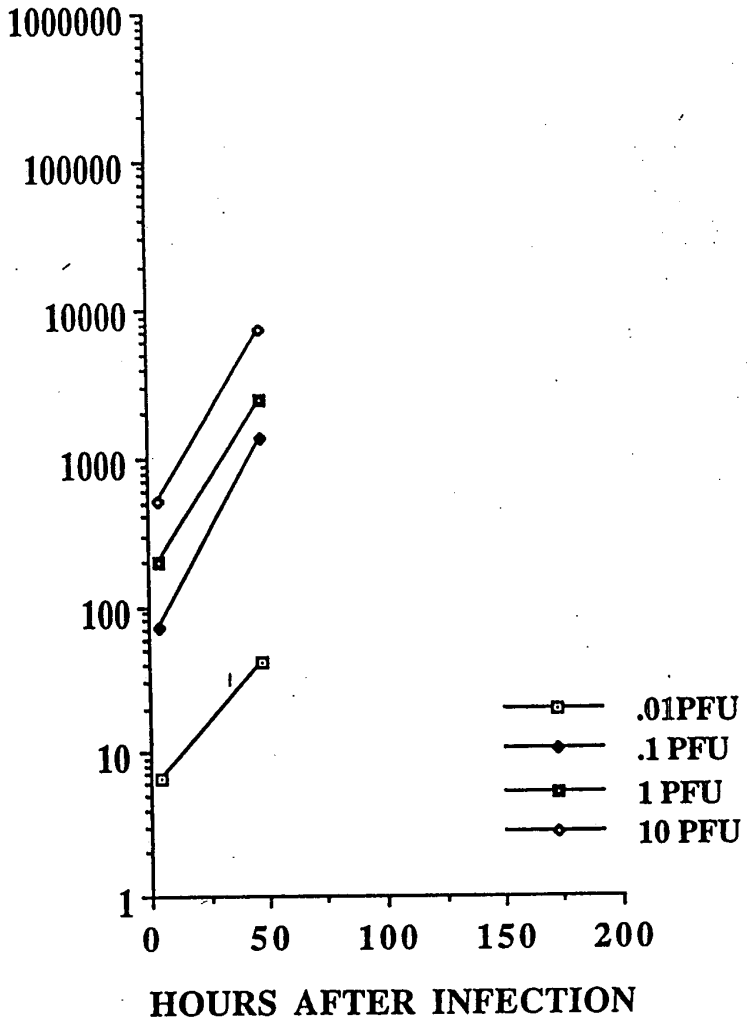
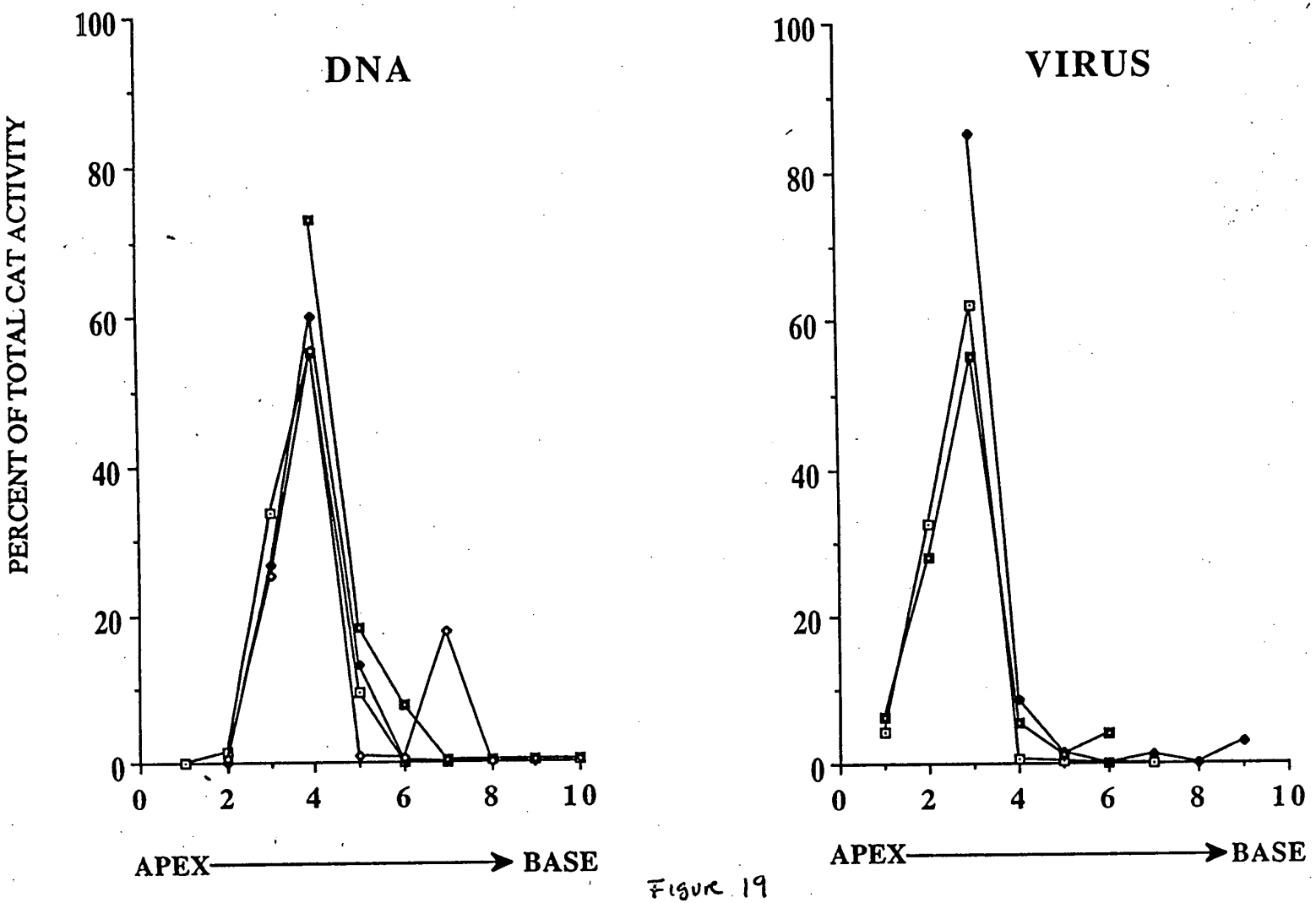


Figure 18(b)

08/166925

DISTRIBUTION OF CAT ACTIVITY FOLLOWING A SINGLE INTRACARDIAC INJECTION



Figur 19

DOSE DEPENDENT CAT EXPRESSION IN THE LEFT VENTRICLE

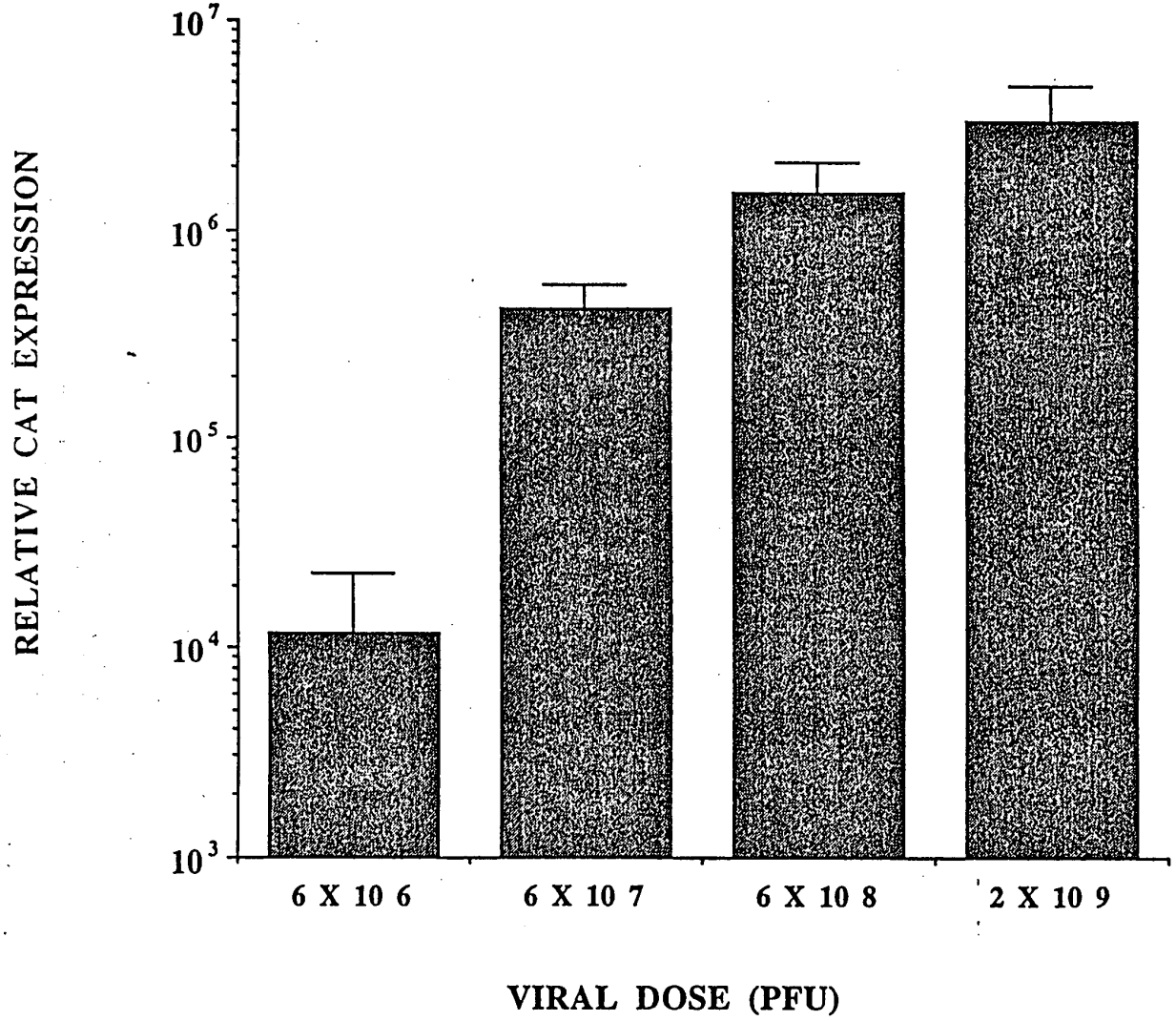


FIGURE 20(a)

08/669925

08/166925

TIME COURSE OF CAT EXPRESSION FOLLOWING INFECTION IN VIVO

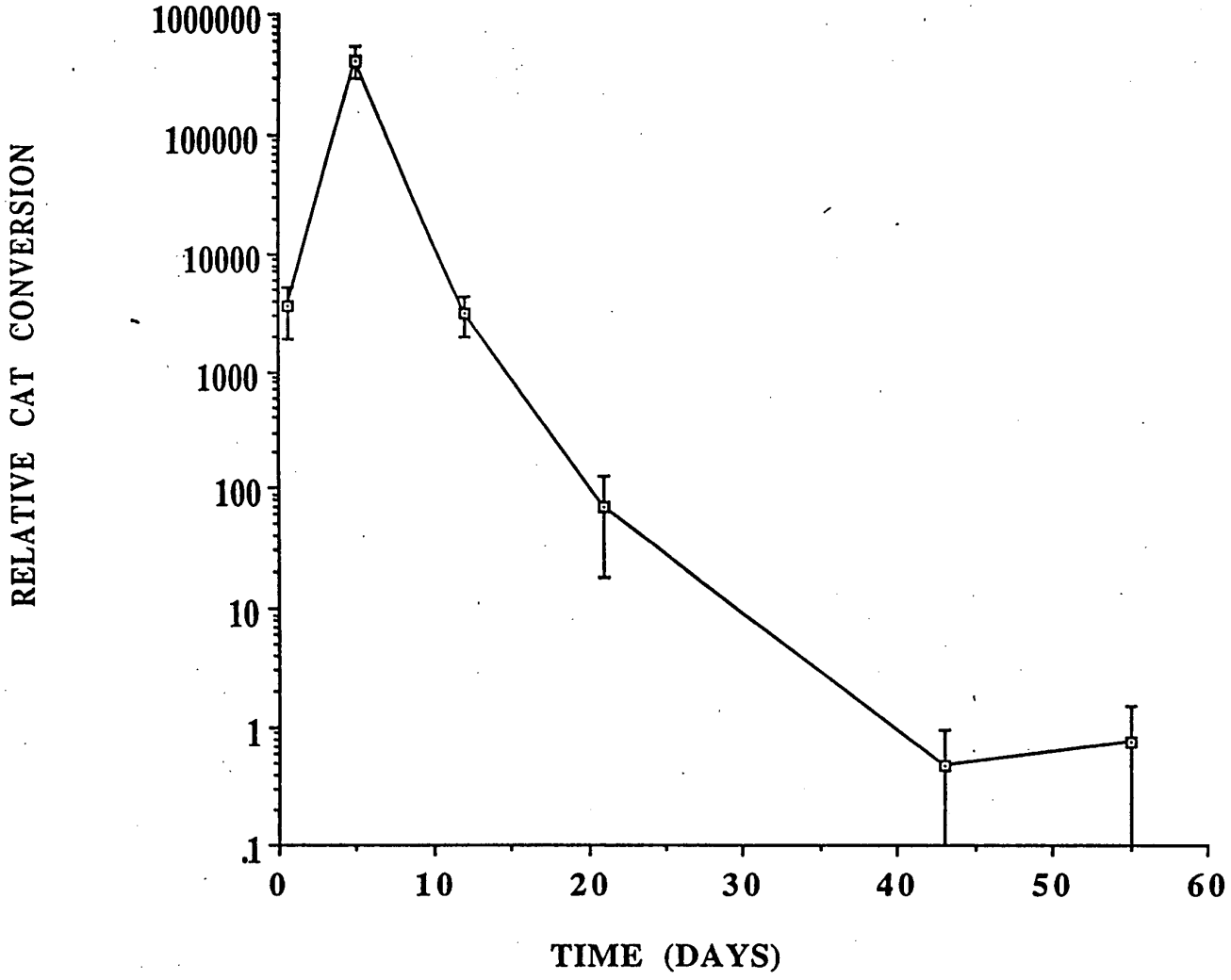


FIGURE 20(b)

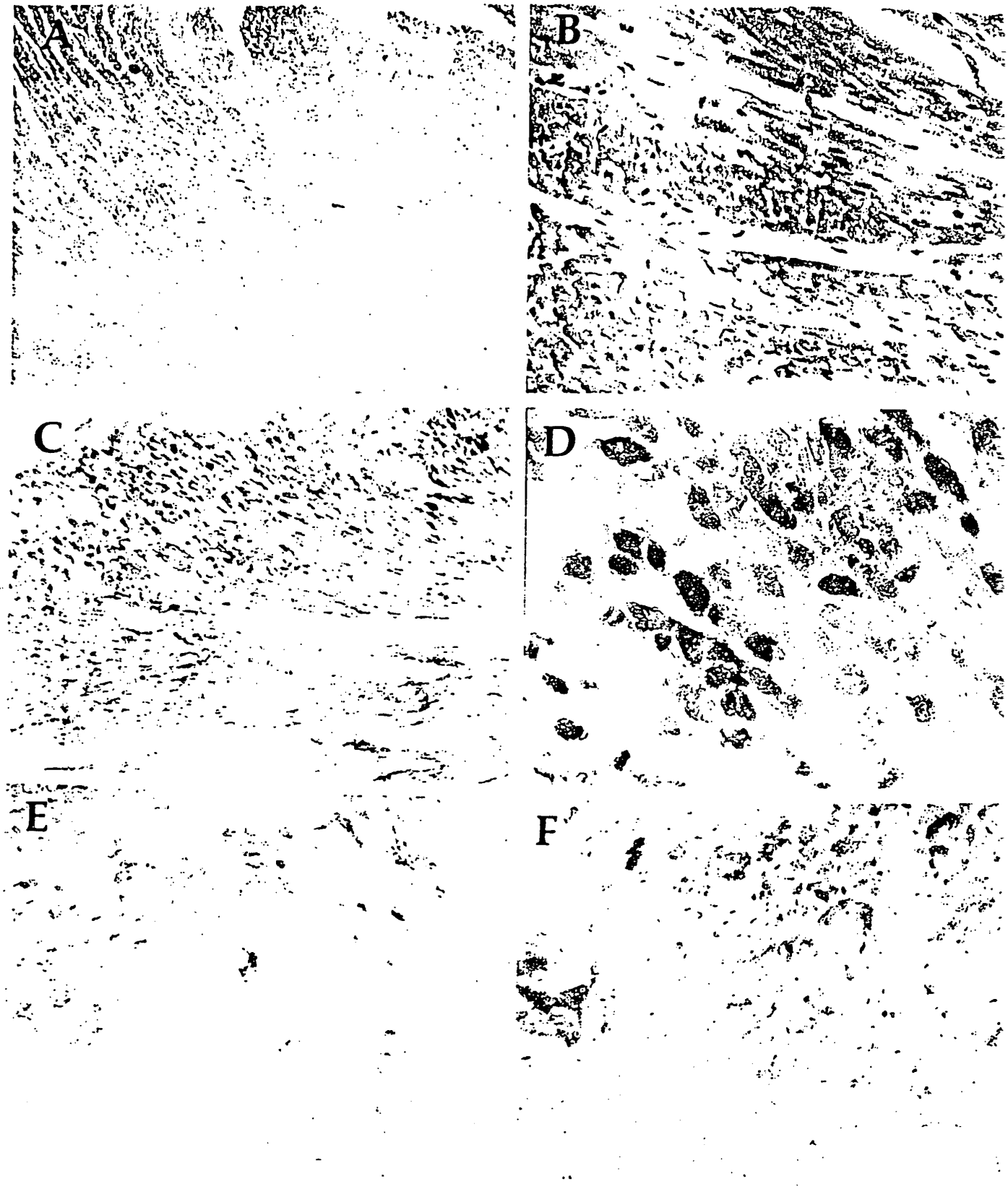


Figure 21

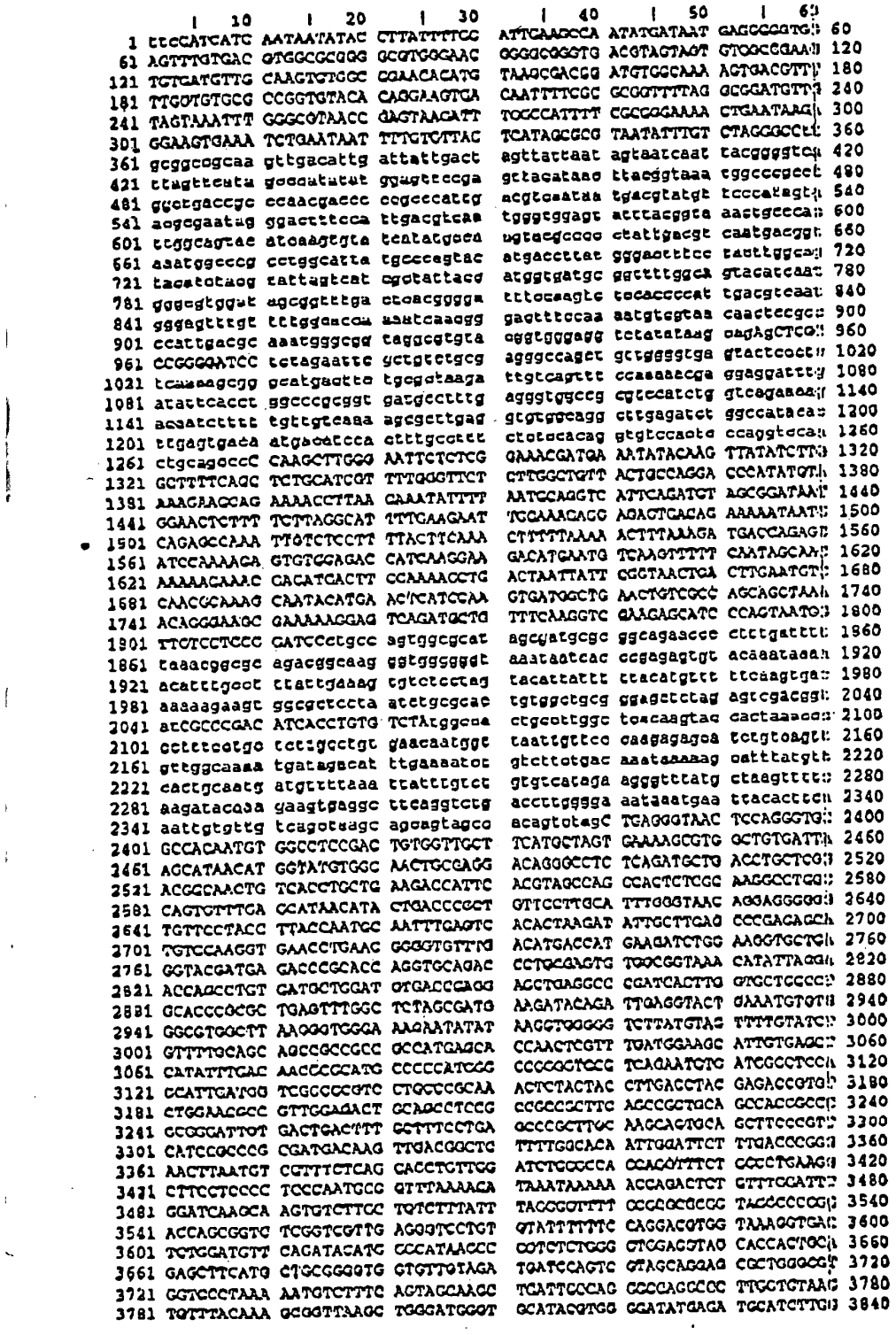


Fig. 22

```
3841 ACTGTATTTT TAGGTTGGCT ATGTTCCCAG CCATATCCCT CCGGGGATTC ATGTTGTGCA 3900
3901 GAACCACCAG CACAGTGTAT CCGGTGCACT TCGGAAATTT GTCATGTAGC TTAGAAGGAA 3960
3961 ATGCGTGGAA GAACTTGGAG ACGCCCTTGT GACCTGCAAG ATTTTCCATG CATTCGTCCA 4020
4021 TAATGATGGC AATGCGCCCA CGGCCGGCGG CCTGGGCGAA GATATTTCTG GGATCACTAA 4080
4081 CGTCATAGTT GTGTTCCAGG ATGAGATCGT CATAGGCCAT TTTTACAAAG CGCGGGCGAA 4140
4141 GGGTGCCAGA CTGCGGTATA ATGGTTGCAT CCCGCCCAGG GCCGTAGTTA CCCTCACAGA 4200
4201 TTTGCATTTC CCACGCTTTG AGTTCAGATG GGGGGATCAT GTCTACCTGC GCGGCGATGA 4260
4261 AGAAAACGGT TTCCGGGGTA GGGGAGATCA GCTGGGAAGA AAGCAGGTTC CTGAGCAGGT 4320
4321 GCGACTTACC GCAGCCGGTG GGCCCGTAAA TCACACCTAT TACCGGGTGC AACTGGTAGT 4380
4381 TAAGAGAGCT GCAGCTGCCG TCATCCCTGA GCAGGGGGGC CACTTCGTTA AGCATGTCCC 4440
4441 TGACTCGCAT GTTTTCCCTG ACCAAATCCG CCAGAAGGCG CTCGCCGCCC AGCGATAGCA 4500
4501 GTTCTTGCAA GGAAGCAAAG TTTTTCAACG GTTTGAGACC GTCCGCCGTA GGCATGCTTT 4560
4561 TGAGCGTTTG ACCAAGCAGT TCCAGGCGGT CCCACAGCTC GGTCACCTGC TCTACGGCAT 4620
4621 CTCGATCCAG CATATCTCCT CGTTTCGCGG GTTGGGGCGG CTTTCGGTGT ACGGCAGTAG 4680
4681 TCGGTGCTCG TCCAGACGGG CCAGGGTCAT GTCTTTCCAC GGGCGCAGGG TCCTCGTCAG 4740
4741 CGTAGTCTGG GTCACGGTGA AGGGGTGCGC TCCGGGCTGC GCGCTGGCCA GGGTGCGCTT 4800
4801 GAGGCTGGTC CTGCTGGTGC TGAAGCCCTG CCGGTCTTCG CCCTGCGCGT CGGCCAGGTA 4860
4861 GCATTTGACC ATGGTGTCAT AGTCCAGCCC CTCGCGCGGC TGGCCCTTGG CGCGCAGCTT 4920
4921 GCCCTTGGAG GAGGCGCCGC ACGAGGGGCA GTGCAGACTT TTGAGGGCGT AGAGCTTGGG 4980
4981 CGCGAGAAAT ACCGATTCCG GGGAGTAGGC ATCCGCGCCG CAGGCCCCGC AGACGGTCTC 5040
5041 GCATTCCACG AGCCAGGTGA GCTCTGGCCG TTCGGGGTCA AAAACCAGGT TTCCCCCATG 5100
5101 CTTTTTGATG CGTTTCTTAC CTCTGGTTTC CATGAGCCGG TGTCCACGCT CGGTGACGAA 5160
5161 AAGGCTGTCC GTGTCCCCGT ATACAGACTT GAGAGGTCGA GCGATGCCCT TGAGAGCCTT 5220
5221 CAACCCAGTC AGCTCCTTCC GGTGGGCGCG GGGCATGACT ATCGTCGCCG CACTTATGAC 5280
5281 TGTCTTCTTT ATCATGCAAC TCGTAGGACA GGTGCCGGCA GCGCTCTGGG TCATTTTCGG 5340
5341 CGAGGACCGC TTTCGCTGGA GCGCGACGAT GATCGGCCTG TCGCTTGCGG TATTCGGAAT 5400
5401 CTTGCACGCC CTCGCTCAAG CCTTCGTCAC TGGTCCCGCC ACCAAACGTT TCGGCGAGAA 5460
5461 GCAGGCCATT ATCGCCGGCA TGGCGGCCGA CGCGCTGGGC TACGTCTTGC TCGCGTTCGG 5520
5521 GACCCGAGGC TGGATGGCCT TCCCCATTAT GATTCTTCTC GCTTCCGGCG GCATCGGGAT 5580
5581 CCCCGCGTTG CAGGCCATGC TGTCCAGGCA GGTAGATGAC GACCATCAGG GACAGCTTCA 5640
5641 AGGATGGCTC GCGGGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCC 5700
5701 TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA 5760
5761 AAGATACCAG GCGTTTCCCC CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC CGACCCTGCC 5820
5821 GCTTACCGGA TACCTGTCCG CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC 5880
5881 ACGCTGTAGG TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA 5940
5941 ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC 6000
6001 GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG 6060
6061 GTATGTAGGC GGTGCTACAG AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACACTAGAAG 6120
6121 GACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG 6180
6181 CTCTTGATCC GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA 6240
6241 GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA 6300
6301 CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT 6360
6361 CTTCACCTAG ATCCTTTTAA ATTAAAAATG AAGTTTTAAA TCAATCTAAA GTATATATGA 6420
6421 GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG 6480
6481 TCTATTTCGT TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA 6540
6541 GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC 6600
6601 AGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC 6660
6661 TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC 6720
6721 AGTTAATAGT TTGCGCAACG TTGTTGCCAT TGCTGCAGGC ATCGTGGTGT CACGCTCGTC 6780
6781 GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC 6840
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6901 GGCCGCAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC 6960
6961 ATCCGTAAGA TGCTTTTCTG TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG 7020
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7081 CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT 7140
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7201 ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA 7260
7261 AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA 7320
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7381 AAATAAACAA ATAGGGGTTC CGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTCTAAGA 7440
7441 AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT ATCACGAGGC CCTTTCGTCT 7500
7501 TCAAGAA                                                        7507
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